

CLAIMS

What is claimed is:

1. A method for the production of a monoterpene comprising:
  - a) providing a transformed C1 metabolizing host cell comprising:
    - (i) suitable levels of geranyl pyrophosphate; and
    - (ii) at least one isolated nucleic acid molecule encoding a cyclic terpene synthase under the control of suitable regulatory sequences;
  - 10 (b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby a monoterpene compound is produced.
2. A method according to Claim 1 wherein the C1 carbon substrate is selected from the group consisting of methane, methanol, formaldehyde, 15 formic acid, methylated amines, methylated thiols, and carbon dioxide.
3. A method according to Claim 1 wherein the C1 metabolizing host cell is a methylotroph selected from the group consisting of *Methylomonas*, *Methylobacter*, *Methylcoccus*, *Methylosinus*, *Methylocyctis*, *Methylomicrobium*, *Methanomonas*, *Methylophilus*, 20 *Methylobacillus*, *Methylobacterium*, *Hyphomicrobium*, *Xanthobacter*, *Bacillus*, *Paracoccus*, *Nocardia*, *Arthrobacter*, *Rhodopseudomonas*, *Pseudomonas*, *Candida*, *Hansenula*, *Pichia*, *Torulopsis*, and *Rhodotorula*.
4. A method according to Claim 1 wherein C1 metabolizing host is a methanotroph.
- 25 5. A method according to Claim 4 wherein the methanotroph is selected from the group consisting of *Methylomonas*, *Methylobacter*, *Methylcoccus*, *Methylosinus*, *Methylocyctis*, *Methylomicrobium*, and *Methanomonas*.
6. A method according to Claim 2 wherein the C1 carbon 30 substrate is selected from the group consisting of methane and methanol and the C1 metabolizing host cell is a methanotroph selected from the group consisting of *Methylomonas*, *Methylobacter*, *Methylcoccus*, *Methylosinus*, *Methylocyctis*, *Methylomicrobium*, and *Methanomonas*.
7. A method according to Claim 6 wherein the obligate 35 methanotroph is a high growth methanotrophic strain which comprises a functional Embden-Meyerof carbon pathway, said pathway comprising a gene encoding a pyrophosphate dependent phosphofructokinase enzyme.

8. A method according to Claim 7 wherein the high growth methanotrophic bacterial strain optionally contains at least one gene encoding a fructose bisphosphate aldolase enzyme.
9. A method according to Claim 7 wherein the high growth methanotrophic bacterial strain optionally contains a functional Entner-Douderoff carbon pathway.
10. A method according to Claim 9 wherein the high growth methanotrophic bacterial strain optionally contains at least one gene encoding a keto-deoxy phosphogluconate aldolase.
11. A method according to Claim 10 wherein the high growth methanotrophic bacterial strain is *methylomonas* 16a having the ATCC designation ATCC PTA 2402.
12. A method according to Claim 1 wherein the cyclic terpene synthase is selected from the group consisting of limonene synthase, pinene synthase, bornyl synthase, phellandrene synthase, cineole synthase, and sabinene synthase.
13. A method according to Claim 1 wherein the monoterpane is selected from the group consisting of limonene, pinene, bornyl diphosphate,  $\beta$ -phellandrene, 1,8-cineole, and sabinene.
14. A method according to Claim 1 wherein the cyclic terpene synthase is limonene synthase, the monoterpane is limonene and the recombinant host is *Methylomonas*.
15. A method according to Claim 14 wherein the limonene synthase has the amino sequence as set forth in SEQ ID NO:6.
16. A method according to Claim 14 wherein the limonene synthase is encoded by the gene as described in the sequences selected from the group consisting of Genbank Acc #AF317695, Genbank Acc # AB005235, Genbank Acc # AF241790, Genbank Acc # AF233894, Genbank Acc # AF139207, Genbank Acc # AF175323 and Genbank Acc # L13459.
17. A method according to Claim 13 wherein the pinene synthase is encoded by the gene as described in sequences selected from the group consisting of Genbank Acc # AF276072, and Genbank Acc # U87909.
18. A method according to Claim 13 wherein the bornyl synthase is encoded by the gene as described in Genbank Acc # AF051900.
19. A method according to Claim 13 wherein the phellandrene synthase is encoded by the gene as described in Genbank Acc # AF139205

20. A method according to Claim 13 wherein the cineole synthase is encoded by the gene as described in Genbank Acc # AF051899.
21. A method according to Claim 13 wherein the sabinene synthase is encoded by the gene as described in Genbank Acc  
5 # AF051901
22. A method according to Claim 1 wherein the suitable levels of geranyl pyrophosphate are provided by the expression heterologous upper pathway isoprenoid pathway genes.
23. A method according to Claim 22 wherein said upper pathway  
10 isoprenoid genes encode enzymes selected from the group consisting of D-1-deoxyxylulose-5-phosphate synthase (DXS); D-1-deoxyxylulose-5-phosphate reductoisomerase (DXR); 2C-methyl-d-erythritol cytidyltransferase (IspD), 4-diphosphocytidyl-2-C-methylerythritol kinase (IspE); 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase (IspF), CTP  
15 synthase (IspA) and Geranyltranstransferase (PyrG).